SEQUENCE LISTING

<110> Yoshinori Watanabe

<120> Novel centromeric protein SHUGOSHIN

<130> 4439-4043

<150> JP2003-401943
<151> 2003-12-01

<150> JP2004-279450
<151> 2004-09-27

<160> 45

<170> PatentIn version 3.1

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gtgaattact cattgccgca aaaaaatatc accatctttt caaaggaatt aaaagaaaac 660

gaatttgaat ccatcaacga gggcgaaact gaagaagaaa aggctaaaac atcaaatgtt 720

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ggagacagct ccccatgtga ttttgaagaa tctcaaccaa ggattaatgg acgtgaaaaa 840

ctaagacgat cagtcaaagt gataaactat gcaataccca gtttgcgaac taaactacga 900

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            20                  25                  30

Ile Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn
        35                  40                  45

Glu Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser Tyr Leu
    50                  55                  60

Val Lys Leu Glu Ala Arg Phe Arg Asn Gln Ser Gln Thr Glu Asp Leu
65                  70                  75                  80

Leu Lys Asn Phe Phe Pro Glu Ile Gln Thr Ile His Lys Lys Ile Ser
                85                  90                  95

Gln Val Gln Ser Leu Leu Lys Ile Ile Glu Lys Lys Cys Ser Ser Asp
            100                 105                 110

Phe Leu Glu Ala Asn Val Lys Ser Gln Phe Thr Thr Cys Glu Asn Lys
        115                 120                 125

Asp Ser Lys Glu Asp Tyr Gln Ile Leu His Asn Lys Arg Leu Glu Tyr
    130                 135                 140

Val Ser Phe Asn Asp Glu Leu Lys Ser Leu Glu Thr Gly Gln Pro Leu
145                 150                 155                 160

Tyr Cys Phe Gln Asp Phe Gln Lys Lys Val His Gly Pro Pro Ala Leu
                165                 170                 175

Ser Glu Lys Pro Gly Lys Cys Ile Leu Lys Asp Lys Thr Asn Ala His
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Val Asn Lys Ile Pro Gln Asp Glu Val Asn Tyr Ser Leu Pro Gln Lys
        195                 200                 205
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Asn Ile Thr Ile Phe Ser Lys Glu Leu Lys Glu Asn Glu Phe Glu Ser
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Ile Asn Glu Gly Glu Thr Glu Glu Glu Lys Ala Lys Thr Ser Asn Val
225                 230                 235                 240

Cys Val Cys Ile Pro Cys Lys Ser Ala Glu Gln Ile Thr Asp Leu Lys
                245                 250                 255

Gly Gln Ala Thr Gly Asp Ser Ser Pro Cys Asp Phe Glu Glu Ser Gln
            260                 265                 270

Pro Arg Ile Asn Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile
        275                 280                 285

Asn Tyr Ala Ile Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe Asp
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35 40 45

Asn Ile Asp Leu Arg Thr Thr Ala Ile Asn Leu Glu Glu Gln Leu Glu
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Thr Val Gln Asn Glu Asn Glu Glu Asn Lys Thr Lys Leu Ala Ala Leu
65 70 75 80

Leu Asn Arg Phe His Glu Glu Thr Asp Asn Phe Leu Ser Lys Leu Ser
85 90 95

Leu Cys Gln Gln Glu Ile Gln Asp Thr Phe Lys Pro Val Glu Ala Asn
100 105 110

Leu Ala Tyr Asp Val Asp Thr Asp Ser Glu Asp Leu Asp Glu Glu Ser
115 120 125

Val Val Lys Asp Thr Glu Glu Ile Ile Glu Gln Ala Gln His Asp Val
130 135 140

Ser Leu Arg Asn Leu Ser Gly Ile Glu Asp Glu Asn Ile Ile Asp Asp
145 150 155 160

Gly Glu Thr Ala Ile Asn Glu Gln Lys Lys Arg Glu Ala Asn Val Phe
165 170 175

Ser Asp Thr Gln Ser Ala Pro Gln Leu Lys Ser Gly Lys Ala Leu Pro
180 185 190

Ala Asp Phe Glu Asn Pro Tyr Asn Leu Ser Asn Ser Lys Pro Val Asn
195 200 205

Asn Asn Asn Glu Asp Arg Val Glu Ala Val Thr Ser Glu Asn Lys Ser
210 215 220

Ile Asp Ser Ala Pro Gln Glu Lys Asn His Glu Tyr Glu Ile Val Ser
225 230 235 240

Pro Lys Ser Leu Ser Asn Lys Ile Asn Asn Gln Ala Ala Ala Gln Arg

245 250 255

Arg Thr Glu Glu Asp Asn Ala Asn Gly Val Ala Gln Glu Glu Asn Glu
260 265 270

Gly Ser Gln Glu Ala His Phe His Ser Arg Ile Gln Ser Asp Thr Val
275 280 285

Ile Gln Ser Thr Pro Thr Lys Arg Lys Trp Asp Val Asp Ile Gln Asn
290 295 300

Lys Gln Ile Asn Leu Ala Ser Ala Ala Thr Asn Val Thr Gly Tyr Val
305 310 315 320

Ser Glu Thr Asp Ser Arg Pro Asn Arg Ala Asn Ser Leu Asp Ser Ala
325 330 335

Val Leu Leu Val Gln Ser Ser Asn Lys Ser Asn Arg Asn Gly His His
340 345 350

Ile Ser Asp Pro Asn Leu Asn Ser Ser Ile Ser Leu Lys Phe Ala Pro
355 360 365

Glu Asp Thr Ala His Asn Ser Leu Thr Ser Gln Glu Asn Val Gly Pro
370 375 380

Gln Val Thr Thr Thr Ser Leu Ser Asn Met Thr Val Ala Glu Ser Pro
385 390 395 400

Arg Thr Asp Thr Pro Arg Glu Ile Asn Gly Leu Val Asp Ser Ser Val
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Thr Asn Gly Asn Glu Lys Phe Ser Val Glu Ile Met Asn Asp Ser Asn
420 425 430

Lys Ile Gly Leu Asn Pro Lys Ser Phe Thr Asp Glu Glu Arg Glu Ile
435 440 445

Leu Thr Leu Phe Arg Asn Pro Pro Met Arg Leu Ser Ser Glu Pro Pro
450 455 460

Ser Ser Asn Gly Phe Ser Ile Ala His Pro Asn Asn Ser Pro Leu Arg
465 470 475 480

Pro Pro Ser Leu Gln Gly Ile Leu Asn Ala Glu Asp Arg Pro Tyr Glu
485 490 495

Ile Glu Pro Ser Arg Ser Ser Phe Ala Thr Asn Asp Thr Gly Ser Tyr
500 505 510

Asn Asn Leu Glu Leu Leu Ser Ser Val Thr Asn Leu Lys Ser Pro Asn
515 520 525

Glu Asn Asp Arg Val Thr Lys Thr Gln Ser Arg Arg Glu Thr Lys Val
530 535 540

Lys Arg Arg Arg Lys Ala Arg Ile Gln Glu Thr Ser Glu Glu Ser Thr
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Val Val Asn Glu Pro Asn Glu Lys Pro Asp Gly Arg Ser Arg Arg Glu
565 570 575

Arg Lys Lys Val Asn Tyr Ala Leu Pro Gly Leu Arg Thr Lys Leu Arg
580 585 590

Arg Asn Phe Asp Leu Pro Ser Asp His Val Lys Ala Lys Lys Thr Arg
595 600 605

Arg Ala Pro Lys Asn Ser Glu Asn Asp Ser Ala Thr Lys Thr Glu Thr
610 615 620

Ala Asn Ile Thr Ser Glu Ala Pro Thr Thr Ser Glu Val Thr Leu Glu
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Asn Ser Glu Thr Leu Asn Leu
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gaaaacatca gacagtcgta ttcgaggcaa aactccctgc tggccaagga taactccata 180

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<211> 590
<212> PRT
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            20                  25                  30

Met Asp Leu Glu Ser Gln Lys Val Glu Asn Ile Arg Gln Ser Tyr Ser
        35                  40                  45

Arg Gln Asn Ser Leu Leu Ala Lys Asp Asn Ser Ile Leu Lys Ile Lys
    50                  55                  60

Val Asn Ser Leu Glu Lys Lys Ile Ser Gln Leu Val Gln Glu Asn Val
65                  70                  75                  80

Thr Leu Arg Ser Lys Thr Ser Ile Ser Glu Ala Ile Tyr Arg Glu Arg
                85                  90                  95

Leu Ser Asn Gln Leu Gln Val Ile Glu Asn Gly Ile Ile Gln Arg Phe
            100                 105                 110

Asp Glu Ile Phe Tyr Met Phe Glu Asn Val Arg Lys Asn Glu Asn Leu
        115                 120                 125

Pro Ser Ser Ser Leu Arg Thr Met Leu Lys Arg Thr Ser Ser Arg Ser
    130                 135                 140

Arg Ser Cys Ser Leu Ser Ser Pro Thr Tyr Ser Lys Ser Tyr Thr Arg
145                 150                 155                 160

Leu Ser Asn His Glu Asn Asn Leu Ser His Glu Ser Ser Phe Asn Lys
                165                 170                 175

Asp Asp Gly Pro Asp Leu Glu Pro Lys Ala Lys Lys Arg Lys Ser Ser
            180                 185                 190

Arg Arg Gln Ser Met Phe Val Ser Thr Ser Leu Glu Pro Glu Asp Glu
        195                 200                 205
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Thr Gly Glu Asn Glu Pro Met Met Glu Asn Ser Ser Val Glu Val Pro
    210                 215                 220

Ala Glu Ser His Glu Ser Ala Gln Val Glu Glu Thr Ile Asp Ala Leu
225                 230                 235                 240

Asn Pro Glu Glu Glu Asn Ser Asp Ser Val Ser Asn Phe Thr Asn Ser
                245                 250                 255

Ile Ile Glu Tyr Ser Ile Pro Glu Glu Asn Pro Thr Glu Pro Glu His
            260                 265                 270

Ser Ser Ser Lys Leu Glu Ile Phe Asn Asp Ser Thr Asn Met Leu Ser
        275                 280                 285

Thr Val Pro Ser Asn Pro Leu Pro Leu Pro Leu Pro Gly Pro Ser Ala
    290                 295                 300

Thr Leu Pro Thr Thr Thr Ser Asp Ala Ser Thr Val Tyr Pro Ser Ser
305                 310                 315                 320

Ser Ser Ser Thr Asn Ser His Pro Lys Thr Lys Ile Lys His Ser Met
                325                 330                 335

Lys Pro Pro Arg Ile Glu Leu Lys Lys Lys Val Ile Asp Glu Val Met
            340                 345                 350

Pro Val Ser Asn Met Ser Ser Asn Ser Glu Ile Ser Phe Thr Arg Thr
        355                 360                 365

Arg Arg Thr Arg Gly Lys Ala Val Asp Tyr Thr Leu Pro Ser Leu Arg
    370                 375                 380

Ala Lys Met Arg Arg Pro Ser Glu Lys Leu Val Asp Ala Thr Thr Val
385                 390                 395                 400

Ile Asp Ile His Asp Leu Gln Val Ser Lys Arg Asn Arg Glu Thr Ser
                405                 410                 415

His Lys Arg Lys Ser Leu Ser Gln Asp Ser Ile Pro Asp Glu Pro Gln
            420                 425                 430
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Leu Arg Glu Val Val Val Ser Lys Asp Tyr Gly Thr Pro Lys Gly Lys
435 440 445

Lys Thr Glu Asp Glu Ile His Glu Asp Thr Ala His Leu Met Thr Thr
450 455 460

Ser Asn Asn Asn Ser Asn Asn Lys Asn Glu Lys Lys Leu Thr Ser Asn
465 470 475 480

Asn Ser Pro Lys Lys Ser Ser Pro Leu Leu Asp Ile Thr Asn Lys Ser
485 490 495

Glu Asn Lys Lys Lys Ser Thr Arg Thr Lys Lys Leu Phe Lys Asn Ala
500 505 510

Ile Val Asn Asn Leu Ser Asp Glu Asn Ser Thr Thr Arg Pro Ser Lys
515 520 525

Ser Ser Lys Gly Thr Ser Asn Asn Asn Asn Asn Tyr Asn Asn Phe Asp
530 535 540

Asn Asn Asn Ser Asn Ile Asn Asn Val Asn Asn Lys Ser Val Ser Phe
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<212> DNA
<213> Neurospora crassa

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Ile Ala Arg Val Asn Ser Thr Gln Ser Leu Arg Ile Arg Gly Leu Glu
35 40 45

Asn Glu Cys Ala Arg Leu Leu Ser Glu Asn Leu Glu Leu Arg Gly Gln
50 55 60

Val Leu Arg Leu Glu Lys Glu Leu Gln Asp Asn Ala Ala Arg Arg Val
65 70 75 80

Ala Asp His Ala Leu Glu Val Lys Ala Lys Met Glu Thr Gln Leu Ala
85 90 95

Glu Leu Ser Ser Leu Leu Ala Ser Leu Gly Glu Pro Pro Ser Lys Arg
100 105 110

Arg Leu Ser Glu Glu Arg Arg Tyr Ala Gln Pro Arg Pro Ser Val His
115 120 125

Arg Ser Pro Pro Leu Arg Arg Ala Arg Gln Glu Ala Asp Gln Glu Leu
130 135 140

Leu Ala Glu Gln Glu Gly Arg Leu Pro Pro Ile Tyr Glu Asn Lys Thr
145 150 155 160

Tyr Ala Arg Ala Thr Met Asn Ser Glu Glu Ile Leu Ala Leu Cys Met
165 170 175

Gln Ala Asp Asp Ser Asn Asp Ser Pro Asp Ile Gly Pro Pro Pro Val
180 185 190

Ser Arg Phe Val Glu Asp Asp Met Val Ile Pro Cys Ser Pro Ser Pro
195 200 205

Asn Lys Asn Ala Glu Ala Glu Glu Thr Glu Thr Thr Glu Gln Val Glu
210 215 220

Glu Ser Pro Arg Ala Leu Gln Val Pro Pro Ser Leu Ser Pro Pro Lys
225 230 235 240

Leu Asp Tyr Asp Arg Arg Pro Asn Met Ile Leu Phe Ser Pro Pro Lys
245 250 255

Glu Ser Arg Val Ala Glu Pro Ser Lys Met Phe Ser Pro Pro Pro Met
260 265 270

Glu Pro Pro Lys Gln Ser Thr Ser Ala Val Pro Ser Glu Thr Ile Arg
275 280 285

Ala Gly Leu Lys Arg Lys Leu Asn Gly Asp Asn Gln Asn Glu Pro Asn
290 295 300

Lys Ala Thr Lys Leu Gln Gln Gly Lys Glu Asn Gly Asn Glu Thr Gly
305 310 315 320

Ile Lys Lys Gly Leu Ser Ala Arg Asp Pro His Lys Arg Lys Ser Ile
325 330 335

Lys Glu Thr Ala Thr Lys Pro Arg Ala Pro Leu Ser Ala Lys Ser Thr
340 345 350

Asn Glu His Ile Val Ser Pro Lys Lys Pro Ala Lys Pro His Gln Val
355 360 365

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Ala Asp Asp Phe Lys Pro Val Lys Val His Lys Ala Ser Lys Gly Lys
    370                 375                 380

Glu Lys Val Asp Leu Pro Ala Pro Asp Lys Lys Ser Ala Val Glu Glu
385                 390                 395                 400

Thr Gln Gly Asn Ser Thr Ser Ala Phe Thr Lys Val Glu Ile Leu Pro
                405                 410                 415

Pro Ala Leu Glu Pro Thr Pro Glu Val Ala Glu Ile Pro Glu Thr Asp
            420                 425                 430

Ile Leu Ile Thr Pro Gly Thr Pro Glu Arg Ala Ser Glu Ser Thr Val
        435                 440                 445

Val Thr His Asp Thr Pro Pro Pro Ala His Ile Ser Ser Asn Gly Glu
    450                 455                 460

Thr Ser Arg Pro Ser Arg Arg Ala Arg Ala Ala Ile Ser Tyr Thr Glu
465                 470                 475                 480

Pro Asn Leu Arg Asp Lys Met Arg Arg Pro Thr Lys Glu Leu Phe Asp
                485                 490                 495

Ala Val Ser Gly Glu Gly Lys Phe Leu His Arg Pro Thr Ser Gln Gln
            500                 505                 510

Gln Gln Gln Gln Arg Lys Gly Asp Glu Ser Ala Pro Thr Ser Val Ser
        515                 520                 525

Lys Val Lys Val Glu Pro Ser Pro Ala Val Asp Ile Ser Ser Leu Thr
    530                 535                 540

Ser Ser Ala Leu Phe Glu Lys Glu Lys Glu Lys Glu Pro Gln Pro Asp
545                 550                 555                 560

Glu Gly Ile Leu Ser Pro Asn Gly Ile Leu Pro Ser Ser Val Asp Leu
                565                 570                 575

Gly Arg Arg Arg Arg Ala Ser Ser Phe Ser Thr Ala Ala Pro Ala Met
            580                 585                 590
```

Thr Ile Pro Ser Val Gln Glu Gln Ser Thr Leu Asn Leu Pro Ala Ala
595 600 605

Asp Glu Thr Asp Glu Asn Ala Ala Val Glu Ala Gln Ile Gln Lys Glu
610 615 620

Leu Ser Asn Ser Ile Thr Thr Arg Pro Arg Gly Gly Lys Gly Arg Gln
625 630 635 640

Ser Met Ser Arg Ser Val Pro Thr Ile Pro Thr Glu Asn Tyr Glu His
645 650 655

Glu Asp Ala Gln Leu Ser Thr Asn Ser Ala Ser Val Asp Leu Tyr Asp
660 665 670

Phe Ala Ser Cys Ala Ser Pro Asp Ser Ala Ala Pro Gln Leu Glu Ala
675 680 685

Thr Thr Gly Asp Val Pro Val Asn Lys Lys Ala Pro Lys Gly Ser Arg
690 695 700

Arg Ala Ser Ser Ala Ala Ser Thr Glu Thr Thr Ala Thr Ala Ser Ala
705 710 715 720

Lys Pro Arg Ser Ser Arg Lys Arg Ala Ser Met Leu Val Pro Lys Lys
725 730 735

Ser Leu Trp Ala Glu Glu Leu Ala Gln Glu Glu Glu Asp Glu Glu Asp
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Val Gly Asn Asp Ser Gly Gly Ser Leu Ser Lys Gly Arg Ala Ser Arg
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Arg Arg Ser Met Met Leu
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<211> 1671
<212> DNA
<213> Arabidopsis thaliana

<400> 9

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ttgggggata ttactaattt gcagaatcag aagaatctaa tgaatcaggg agcgaagcat 180

cagcaacaag ctatattaat ctcttctaaa gaaaacgctg aaaatcttca aaaggcactg 240

agaaattctt ctgaaaacac aaagctgatg aaagtcgtca tggagagaga tggaatcaaa 300

agtgatctga agaaacttag gattgaattt cagaaggttc aagaacagaa tttgctactt 360

gcccaggcta acactcgtat cttggcgctg aaggtacttc agcacgaact tggttgcaag 420

aatgggttag tcatggccag gaaaatgctg cttaaggctc aagcaaatgc ttgtggtggg 480

gcttgcaaaa cctttcagcc aaatgatgca gatcatgagc atgcttccgg gagctccaac 540

gctaactcat tgcaaagaaa tgagaaagcc aacagtaaaa ggagagtttc tggaaggaag 600

aatcccgcca attccgaggt attagatata attggcagat cgggagagac atgtcagatg 660

gaagacaaca ttgacaacaa gaagttggtc tctgatagtg acaatgatgc tgaaaaccat 720

ataaatgaca atgtccaaag caaaagatat tgtgcaggaa gacagagtag cagttctaag 780

actcgagaag ccagccaaac agaaaccttg caaaaggtgg ttgacgccaa agaaattaag 840

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ccatctgaaa gcctatacga gtcaaggttc cctttgagaa ggcgttctgc ccggttaaaa 960

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atcaaagaac ctgcaaatcc gcctttgcat gatgacaatg ttgaggagtc tagtcagata 1500

tcatgttcag tttcaatgga gcttaaaaga gaatcaaaga agaaaccaac aggcgacgaa 1560

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<210> 10
<211> 556
<212> PRT
<213> Arabidopsis thaliana

<400> 10

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Val Arg Thr Asn Lys Ala Lys Gly Glu Lys Met Val Leu Glu Pro Pro
            20                  25                  30

Met Asn Ser Ala Gln Arg Arg Lys Leu Gly Asp Ile Thr Asn Leu Gln
        35                  40                  45

Asn Gln Lys Asn Leu Met Asn Gln Gly Ala Lys His Gln Gln Gln Ala
    50                  55                  60

Ile Leu Ile Ser Ser Lys Glu Asn Ala Glu Asn Leu Gln Lys Ala Leu
65                  70                  75                  80

Arg Asn Ser Ser Glu Asn Thr Lys Leu Met Lys Val Val Met Glu Arg
                85                  90                  95

Asp Gly Ile Lys Ser Asp Leu Lys Lys Leu Arg Ile Glu Phe Gln Lys
            100                 105                 110

Val Gln Glu Gln Asn Leu Leu Leu Ala Gln Ala Asn Thr Arg Ile Leu
        115                 120                 125

Ala Leu Lys Val Leu Gln His Glu Leu Gly Cys Lys Asn Gly Leu Val
    130                 135                 140

Met Ala Arg Lys Met Leu Leu Lys Ala Gln Ala Asn Ala Cys Gly Gly
145                 150                 155                 160

Ala Cys Lys Thr Phe Gln Pro Asn Asp Ala Asp His Glu His Ala Ser
                165                 170                 175

Gly Ser Ser Asn Ala Asn Ser Leu Gln Arg Asn Glu Lys Ala Asn Ser
            180                 185                 190
```

Lys Arg Arg Val Ser Gly Arg Lys Asn Pro Ala Asn Ser Glu Val Leu
195 200 205

Asp Ile Ile Gly Arg Ser Gly Glu Thr Cys Gln Met Glu Asp Asn Ile
210 215 220

Asp Asn Lys Lys Leu Val Ser Asp Ser Asp Asn Asp Ala Glu Asn His
225 230 235 240

Ile Asn Asp Asn Val Gln Ser Lys Arg Tyr Cys Ala Gly Arg Gln Ser
245 250 255

Ser Ser Ser Lys Thr Arg Glu Ala Ser Gln Thr Glu Thr Leu Gln Lys
260 265 270

Val Val Asp Ala Lys Glu Ile Lys Gly Asp Ala Arg Phe Ser Leu Thr
275 280 285

Lys His Ser Asp Trp Leu Lys Ser Gln Glu Pro Glu Pro Ser Glu Ser
290 295 300

Leu Tyr Glu Ser Arg Phe Pro Leu Arg Arg Arg Ser Ala Arg Leu Lys
305 310 315 320

Ser Gln Glu Pro Glu Pro Ser Glu Ser Phe His Asp Ser Ile Glu Thr
325 330 335

Thr Lys Arg Arg Arg Ser Ala Ile Arg Ser Ala Met Phe Asn Ile Gln
340 345 350

Glu Leu Gly Val Ile Gln Asn Leu Asn Gly Leu Pro Asp Asp Gln Glu
355 360 365

Ile Ala Ala Lys Ala Arg Cys Ser Ala Arg Glu Gln Ser Thr Gly Ser
370 375 380

Lys Pro Glu Ala Val Glu Pro His Asp Thr Lys Glu Ile Ile Gly Lys
385 390 395 400

Ser Arg Ile Ser Leu Arg Arg Gln Ser Ala Arg Phe Asn Phe Gln Glu
405 410 415

Leu Gly Val Thr Glu Asn Leu Asn Gly Pro His Asp Asp Gln Thr Ile
420 425 430

Ala Ala Asn Ala Arg Cys Cys Ala Ser Glu Gln Ser Ile Gly Ser Lys
435 440 445

Pro Glu Ala Val Glu Pro His Asp Ile Glu Glu Arg Ile Gly Lys Ile
450 455 460

Arg Val Ser Ser Arg Arg Gln Ser Ala Asn Ile Glu Thr Pro Arg Ala
465 470 475 480

Ile Lys Glu Pro Ala Asn Pro Pro Leu His Asp Asp Asn Val Glu Glu
485 490 495

Ser Ser Gln Ile Ser Cys Ser Val Ser Met Glu Leu Lys Arg Glu Ser
500 505 510

Lys Lys Lys Pro Thr Gly Asp Glu Ser Glu Glu Met Arg Lys Thr Thr
515 520 525

Val Gly Arg Pro Ser Arg Gln Ala Ala Glu Lys Ile Lys Ser Tyr Lys
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Glu Pro Ser Leu Lys Glu Lys Met Arg Gly Gly Phe
545 550 555

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<211> 1341

<212> DNA
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gctctagcac accgaaataa actcgtcgag ttgagcggta ttgagattca gaaactgagg 180

attaacttac ggagtgtgca ggaaaagaat ttgcagcttg ctcaggcaaa cagtcagatg 240

ttagcgctca aggatctcca gcatgaactt ggctgcaaga atgctttact taaagtcaag 300

aaacatcttg aggagcaagt acttccacgt acacatcatg aatcgaaaga caaggtttca 360

gcaagcgctt ctgatgggga ttgcaaatcc tttcaggtgc atgacataaa acataaagat 420

accaagagaa agcgaacaac aaggataaaa tcttcagtaa gtgccgacgt caagccaata 480

cctgtgaatg attctaacag taaagctaac cgtaaaagaa gagtttctgg agtaatagat 540

actactggta ttcccgaaga gatctgtcag actgaagatg acattgataa gggggttgtc 600

tctcgagggg taaaccaaga tattgacaat gttgtcaaca agaagtttgt tcctgatgca 660

gcaaacccgg taaaagagag tgtgcatcgc aagaggcaat gtacacgaag gcaatctacc 720

agatttgatg ttcaagaaac taaacaaacg gaaaagttgc ttgagatgga tggtgccaaa 780

gaaagtaaag aaaccgcaag cttctctttg agaagacggt ctgctcggtt aaggcacgaa 840

gaagctgaac catgtaaaag cttacatgag ggagacgaag tcagggagac aatcaagagg 900

agaagagtct ctttaagact gtctgcaagg tttgatatac aagaaccgca tgtgactgaa 960

acctcgaatg ctgacgatgc aagaagcata gtaatcgaag aatctgctgg atcaagatcg 1020

gaatctgtag aaccatccga aagcaggcat gaaacaaaag agataacccg gaaacgcagt 1080

ttctcaacga gaagacaatc aacaaagggt aaatctcaaa ccgatgaagc cattaaagaa 1140

atagcgacag acccatcttt ggtcaacacc atagttcaag agtgtgatca ggaaacagaa 1200

tcaaaggata agcctaaagc tgatgaaaac gaagggatga caagaagatc atctgtggga 1260

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aagatgcgac gaaaatgcta a 1341

<210> 12
<211> 446
<212> PRT
<213> Arabidopsis thaliana

<400> 12

Met Asp Lys Glu Glu Thr Gln Gln Lys Glu Asn Met Leu Phe Ser Ser
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Gln Glu Tyr Ala Ala Lys Leu Gln Lys Ala Phe Pro Leu His Phe Asn
20 25 30

Leu Glu Asn Met Thr Leu Met Lys Ala Leu Ala His Arg Asn Lys Leu
35 40 45

Val Glu Leu Ser Gly Ile Glu Ile Gln Lys Leu Arg Ile Asn Leu Arg
50 55 60

```
Ser Val Gln Glu Lys Asn Leu Gln Leu Ala Gln Ala Asn Ser Gln Met
65                  70                  75                  80

Leu Ala Leu Lys Asp Leu Gln His Glu Leu Gly Cys Lys Asn Ala Leu
                85                  90                  95

Leu Lys Val Lys Lys His Leu Glu Glu Gln Val Leu Pro Arg Thr His
            100                 105                 110

His Glu Ser Lys Asp Lys Val Ser Ala Ser Ala Ser Asp Gly Asp Cys
        115                 120                 125

Lys Ser Phe Gln Val His Asp Ile Lys His Lys Asp Thr Lys Arg Lys
    130                 135                 140

Arg Thr Thr Arg Ile Lys Ser Ser Val Ser Ala Asp Val Lys Pro Ile
145                 150                 155                 160

Pro Val Asn Asp Ser Asn Ser Lys Ala Asn Arg Lys Arg Arg Val Ser
                165                 170                 175

Gly Val Ile Asp Thr Thr Gly Ile Pro Glu Glu Ile Cys Gln Thr Glu
            180                 185                 190

Asp Asp Ile Asp Lys Gly Val Val Ser Arg Gly Val Asn Gln Asp Ile
        195                 200                 205

Asp Asn Val Val Asn Lys Lys Phe Val Pro Asp Ala Ala Asn Pro Val
    210                 215                 220

Lys Glu Ser Val His Arg Lys Arg Gln Cys Thr Arg Arg Gln Ser Thr
225                 230                 235                 240

Arg Phe Asp Val Gln Glu Thr Lys Gln Thr Glu Lys Leu Leu Glu Met
                245                 250                 255

Asp Gly Ala Lys Glu Ser Lys Glu Thr Ala Ser Phe Ser Leu Arg Arg
            260                 265                 270

Arg Ser Ala Arg Leu Arg His Glu Glu Ala Glu Pro Cys Lys Ser Leu
        275                 280                 285
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His Glu Gly Asp Glu Val Arg Glu Thr Ile Lys Arg Arg Arg Val Ser
    290                 295                 300

Leu Arg Leu Ser Ala Arg Phe Asp Ile Gln Glu Pro His Val Thr Glu
305                 310                 315                 320

Thr Ser Asn Ala Asp Asp Ala Arg Ser Ile Val Ile Glu Glu Ser Ala
                325                 330                 335

Gly Ser Arg Ser Glu Ser Val Glu Pro Ser Glu Ser Arg His Glu Thr
            340                 345                 350

Lys Glu Ile Thr Arg Lys Arg Ser Phe Ser Thr Arg Arg Gln Ser Thr
        355                 360                 365

Lys Gly Lys Ser Gln Thr Asp Glu Ala Ile Lys Glu Ile Ala Thr Asp
    370                 375                 380

Pro Ser Leu Val Asn Thr Ile Val Gln Glu Cys Asp Gln Glu Thr Glu
385                 390                 395                 400

Ser Lys Asp Lys Pro Lys Ala Asp Glu Asn Glu Gly Met Thr Arg Arg
                405                 410                 415

Ser Ser Val Gly Arg Pro Ser Arg His Ala Ala Glu Lys Val Gln Ser
            420                 425                 430

Tyr Arg Glu Val Ser Leu Arg Val Lys Met Arg Arg Lys Cys
        435                 440                 445
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<212> DNA
<213> mouse

<400> 13

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gttgcaccgg gccaagtacc cactaacact gctacactac tgagatatta ccaagataac    180

aacaggttgt tagtcttggc tttggaaaat gagaaatcca aagtgagaga agcacaggat    240

gtcatcctgc aactgagaaa agaatgctac taccttactt gtcagctgta tgcattgaaa    300
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gacgtggtct ccagcattga caatacgacc agggacttgt cagggaagtc cttacagcaa 420

attgctgttg aagaaactga ttgtccttac caaaccacag aaccaagtcc tgctgttact 480

ccagagacac agggttgcga ttttgattca ggtaaagttg agtctactga tgaagtctta 540

cccagaacta tatctatccg tcgccattta aggaaagatt ttagtaatat aagccactcc 600

acgactttgg aggattgtaa agccagtcca agagtggcac agtctctgga agttaaagga 660

agtagatgta gagaagtaac cgtaaccctg cacagacttg aaaatgtttg tctgtggaac 720

aaagaccaaa ttagcttatg ttctagactg attaacccag caaagattac tgaaacagaa 780

gtcattttat catctaaacc tgaacaaata gaaagcaagc ataaacgtgc acgaaaaaga 840

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gggaacaaaa acaaagataa gcagggttta ccccctacta cactggatgg aggtattggt 960

tcctgtgatg cttacgattt taatctaaaa gggacggtcc accccacccc tttccgacaa 1020

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cgagactaca gagagtcaga gagagcagtt accaggcctc ggtctaaaag aggacttcag 1200

tacccagatg ggaaagagag gaaggaggtg ctgccatcta cagctcctac tggtatccca 1260

cctgagactc aagagtcacc tcgttgtagc ctaaaggatg tcaccaatat cctgcagtgt 1320

cctagagtga agatcaggaa gccttctctg cctccaaagc ggcgtgaaga cagcccagca 1380

gtggctctga ctaaacgcag gtgtagcacc atcaaaagct ataaagagcc aacactcgct 1440

tcaaagctaa gaagagggga ccctttcacg gacttgtgtt tcttgaattc tcctattttc 1500

aagcagaaaa ggggtatgag atgtcctaaa agaagaacca agcaaacaca gtaa 1554

<210> 14
<211> 517
<212> PRT
<213> mosue

<400> 14

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Asp Ile Lys Asn Arg Met Lys Glu Lys Arg Asn Lys Asn Leu Ala Gly
20 25 30

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Ile Gly Lys Arg Lys Ser Phe Ile Val Ala Pro Gly Gln Val Pro Thr
        35                  40                  45

Asn Thr Ala Thr Leu Leu Arg Tyr Tyr Gln Asp Asn Asn Arg Leu Leu
    50                  55                  60

Val Leu Ala Leu Glu Asn Glu Lys Ser Lys Val Arg Glu Ala Gln Asp
65                  70                  75                  80

Val Ile Leu Gln Leu Arg Lys Glu Cys Tyr Tyr Leu Thr Cys Gln Leu
                85                  90                  95

Tyr Ala Leu Lys Glu Lys Leu Thr Ser Arg Gln Ser Glu Glu Thr Thr
            100                 105                 110

Gln Asn Trp Lys Gly Arg Pro Ser Asp Val Val Ser Ser Ile Asp Asn
        115                 120                 125

Thr Thr Arg Asp Leu Ser Gly Lys Ser Leu Gln Gln Ile Ala Val Glu
    130                 135                 140

Glu Thr Asp Cys Pro Tyr Gln Thr Thr Glu Pro Ser Pro Ala Val Thr
145                 150                 155                 160

Pro Glu Thr Gln Gly Cys Asp Phe Asp Ser Gly Lys Val Glu Ser Thr
                165                 170                 175

Asp Glu Val Leu Pro Arg Thr Ile Ser Ile Arg Arg His Leu Arg Lys
            180                 185                 190

Asp Phe Ser Asn Ile Ser His Ser Thr Thr Leu Glu Asp Cys Lys Ala
        195                 200                 205

Ser Pro Arg Val Ala Gln Ser Leu Glu Val Lys Gly Ser Arg Cys Arg
    210                 215                 220

Glu Val Thr Val Thr Leu His Arg Leu Glu Asn Val Cys Leu Trp Asn
225                 230                 235                 240

Lys Asp Gln Ile Ser Leu Cys Ser Arg Leu Ile Asn Pro Ala Lys Ile
                245                 250                 255
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Thr Glu Thr Glu Val Ile Leu Ser Ser Lys Pro Glu Gln Ile Glu Ser
            260                 265                 270

Lys His Lys Arg Ala Arg Lys Arg Arg Ala Glu Gln Arg Arg Thr Lys
        275                 280                 285

Gln Arg Cys Lys Ser Lys Ser Ser Leu Arg Ser Lys Gly Asn Lys Asn
    290                 295                 300

Lys Asp Lys Gln Gly Leu Pro Pro Thr Thr Leu Asp Gly Gly Ile Gly
305                 310                 315                 320

Ser Cys Asp Ala Tyr Asp Phe Asn Leu Lys Gly Thr Val His Pro Thr
                325                 330                 335

Pro Phe Arg Gln Lys Met Asn Asn Gly Cys Asn Lys Glu Thr Asp Ser
            340                 345                 350

Ser Asn Ser Glu Val Ser Asp Leu Glu Cys Ser Thr Ser Glu Asp Glu
        355                 360                 365

Ser Asp Asp Leu Tyr Leu Pro Pro Ser Lys Arg Leu Arg Asp Tyr Arg
    370                 375                 380

Glu Ser Glu Arg Ala Val Thr Arg Pro Arg Ser Lys Arg Gly Leu Gln
385                 390                 395                 400

Tyr Pro Asp Gly Lys Glu Arg Lys Glu Val Leu Pro Ser Thr Ala Pro
                405                 410                 415

Thr Gly Ile Pro Pro Glu Thr Gln Glu Ser Pro Arg Cys Ser Leu Lys
            420                 425                 430

Asp Val Thr Asn Ile Leu Gln Cys Pro Arg Val Lys Ile Arg Lys Pro
        435                 440                 445

Ser Leu Pro Pro Lys Arg Arg Glu Asp Ser Pro Ala Val Ala Leu Thr
    450                 455                 460

Lys Arg Arg Cys Ser Thr Ile Lys Ser Tyr Lys Glu Pro Thr Leu Ala
465                 470                 475                 480
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Ser Lys Leu Arg Arg Gly Asp Pro Phe Thr Asp Leu Cys Phe Leu Asn
485 490 495

Ser Pro Ile Phe Lys Gln Lys Arg Gly Met Arg Cys Pro Lys Arg Arg
500 505 510

Thr Lys Gln Thr Gln
515

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<211> 3495
<212> DNA
<213> mouse

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ttaaacaatt cttctatttt caagatctct ctaaagcaca acaacagagc attagcgcgg 180

gcccttagta aagagaaaga gaattctcga agaattacta ccgaaaagat gcaattacag 240

aaagaagtag agaaactgaa ttttgagaat acctttcttc gcttaaagtt aaataccttg 300

aataagaagc ttgtagaaat agaatcgcat gtgagcaatg atttgttaac tgcaattgaa 360

ataagcagtc tttctgagtt ccaccaaggt tcttttctcc tgtcagctac caagaaacaa 420

aggaacagta agcagtgcaa gcctgcgcat cttccatatg caagagttct gttaacttca 480

gaaaatgatg atgatgatgg tgctgatgat aaatggcaga caaagtgtaa caacagaact 540

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cagtgcaatt tgaaagcatt ccctcctaaa gaagataatc agaagacatg tgggtcaggt 660

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cctaagagtt ctctgagtga gatgaaaact gctccatctc ccagcctcag aagggaaaaa 780

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gctaatgaaa atgtatgtga ccatgagact cagacaatgt tggacttgaa aaagtctgtc 1740

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gaaaaagaca actttccctt tcatacccaa gcaaataaag aaaccaccag tggaaaccta 1920

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gactgtaaga cccagaatgt tctggatctg cacaagcaaa ttcctgatct ataccctgat 2040

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gatacgcctg ctttttgtaa caaagatagt gcaaagtcgt gtgattataa gtctgaaatg 2280

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caaatacatg aaaatgatag aggaagtaca catgactcat taaataagaa gctctgtcag 2460

aaggttaata tatcaaaaat catttctcaa atgaaccaaa tatatgagac tattaatgaa 2520

gatggaaatg gctttaaaag ctctatcaaa gattgcgaag atattaaaag ttgtgacttt 2580

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gttaaaaaaa caaagagaaa gggatcatgt aaagcaggga gcagtttggc aggagctaag 2700

aacaggtgtg gtttgcagtt aacagactct tcccaggtac agtctgtccc cttagactct 2760

ggcttaagac accatccaaa cgaagcagat tctggtcctg gagagcagac taacctgcca 2820

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aagctccctc tcggttgttc tcctgaaacc cacgggacgg tggagataac acccaacact 3000

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atctttcaag taggtgatgc cgctcatgag aagataacga caggcacacg taatccccac 3300

cacaggacac agaagtcgac accgggtagc agaacgtccc tggtcttggt ggataccagt 3360

tctgtttcag ataccaaccc tgctaacccc gagaatgagt cagaagggca gtcttcacac 3420

ccaatgagaa ggaaaagaca gtgcgtccct ctcaacctga cagagccaag ccttagaagc 3480

aagatgagga gataa 3495

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<212> PRT
<213> mouse

<400> 16

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Arg Arg Val Lys Gly Arg Ile Ala Lys Thr Asn Leu Asn Val Ser Leu
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Ala Ser Lys Ile Lys Ala Lys Ile Leu Asn Asn Ser Ser Ile Phe Lys
35 40 45

Ile Ser Leu Lys His Asn Asn Arg Ala Leu Ala Arg Ala Leu Ser Lys
50 55 60

Glu Lys Glu Asn Ser Arg Arg Ile Thr Thr Glu Lys Met Gln Leu Gln
65 70 75 80

Lys Glu Val Glu Lys Leu Asn Phe Glu Asn Thr Phe Leu Arg Leu Lys
85 90 95

Leu Asn Thr Leu Asn Lys Lys Leu Val Glu Ile Glu Ser His Val Ser
100 105 110

Asn Asp Leu Leu Thr Ala Ile Glu Ile Ser Ser Leu Ser Glu Phe His
115 120 125

Gln Gly Ser Phe Leu Leu Ser Ala Thr Lys Lys Gln Arg Asn Ser Lys
130 135 140

Gln Cys Lys Pro Ala His Leu Pro Tyr Ala Arg Val Leu Leu Thr Ser
145 150 155 160

Glu Asn Asp Asp Asp Asp Gly Ala Asp Asp Lys Trp Gln Thr Lys Cys
165 170 175

Asn Asn Arg Thr Ile Ser Lys Thr Ser Pro Asp Ser Thr Ser Ser Val
180 185 190

Ser Arg Gln Pro Ser Ser Leu His Gln Cys Asn Leu Lys Ala Phe Pro
195 200 205

Pro Lys Glu Asp Asn Gln Lys Thr Cys Gly Ser Gly His Leu Glu His
210 215 220

Thr Ser Ser Val Asp Ile Leu Pro Asn Glu Ser His Ser Asp Gln Ser
225 230 235 240

Pro Lys Ser Ser Leu Ser Glu Met Lys Thr Ala Pro Ser Pro Ser Leu
245 250 255

Arg Arg Glu Lys Leu Ser His Gly Asn Val Thr Met Arg Lys Lys Cys
260 265 270

Val Ser Ser Thr Pro Asp Ile Leu Tyr Val Thr Asp Leu Asp His Gln
275 280 285

Pro Thr Ser Ser Pro Gly Ser Asn Trp Asn Asn Glu Ile His Gly His
290 295 300

Thr Asn Glu Thr Ser Asn Asn Thr Gln Arg Asn Ala Glu Cys Phe Leu
305 310 315 320

Asp Leu Pro Ser Glu Ser Ser Ser Glu Pro Asp Ala Lys Arg Met Glu
325 330 335

Leu Val Gln Lys Asn Thr Asp Ser Phe His Phe Gln Lys Thr Val Tyr
340 345 350

Asp Ala Ala Asp Met Glu Leu Thr Ala Thr Asp Ile Gly Lys Ile Val
355 360 365

Ala Val Ser Lys Ser Lys Lys Asn Gln Asn Lys Lys Lys Ala Asp Cys
370 375 380

Arg Lys Glu Thr Phe Arg Lys Val Lys Gly Ala Ser Ser Asp Lys Lys
385 390 395 400

Arg Glu Ser Ser Lys Arg Glu Cys Lys Asp Gly Ser Glu Val Gly Ala
405 410 415

Glu Glu Glu Ala Asp Ala Ala Arg Ala Glu Arg Gly Ala Gly Val Leu
420 425 430

Asp Gly Arg Gly Asp Ser Glu Glu Pro Asn Cys Ile Ser Ser Thr Glu
435 440 445

Gln Pro Ser Gln Val Asn Thr Gln Lys Lys Arg Thr Leu Gln Asn Ser
450 455 460

Ser Asp Gln Glu Asn Ile Gln Asn Thr Lys Arg Arg Gln Thr Tyr Thr
465 470 475 480

Thr Asp Glu Gln Glu Glu Thr Asn Pro Phe Ser Arg His Ser Val Lys
485 490 495

Phe Leu Gln Asp Gly Lys Phe Asp Leu Cys Gln Lys Thr Leu His His
500 505 510

Asn Leu Ser Lys Pro Ser Arg Gln Thr Phe Val Ile Arg Lys Ser Glu
515 520 525

Lys Asp Asn Leu Phe Pro Asn Gln Glu Asp Lys Asp Thr Ile Ser Glu
530 535 540

Asn Leu Glu Val Thr Asn Glu Phe His Ile Asp Asp Leu Ser Ile Glu
545 550 555 560

Ala Asn Glu Asn Val Cys Asp His Glu Thr Gln Thr Met Leu Asp Leu

565 570 575

Lys Lys Ser Val Ser Ala Gln Gln Asn Gln Thr Lys Ile Asn Lys Thr
580 585 590

Lys Gln Lys Ile Asn Arg Arg Thr Lys Ile Ile Ser Val Met Ser Gln
595 600 605

Val Tyr Glu Asp Asn Asp Lys Asp Ile His Val Leu Glu Lys Asp Asn
610 615 620

Phe Pro Phe His Thr Gln Ala Asn Lys Glu Thr Thr Ser Gly Asn Leu
625 630 635 640

Glu Ser Ser Lys Glu Phe Glu Ser Pro Leu Leu Phe Thr Arg Asp Asn
645 650 655

Gly Ser Leu Arg Asp Cys Lys Thr Gln Asn Val Leu Asp Leu His Lys
660 665 670

Gln Ile Pro Asp Leu Tyr Pro Asp Arg Asn Glu Ser Gln Ile Ser Lys
675 680 685

Ile Pro Arg Gln Lys Val Asn Arg Lys Thr Glu Val Ile Ser Gly Val
690 695 700

Lys Cys Phe Ser Asn Asp Gln Gly Val His Cys Ser Glu Lys Asp Lys
705 710 715 720

Ser Leu Leu Leu Gln Lys Asp Lys Asp Phe Pro Gly Thr Leu Lys Asp
725 730 735

Leu Ser Glu Phe Asp Thr Pro Ala Phe Cys Asn Lys Asp Ser Ala Lys
740 745 750

Ser Cys Asp Tyr Lys Ser Glu Met Leu Leu Gly Leu Lys Lys His Asp
755 760 765

Pro Asn Met Gln Pro Ala Cys Gln Asp Asp Ser Lys Ala Gly Lys Lys
770 775 780

Leu Arg Gln Lys Val Asn Arg Lys Thr Glu Ile Ile Ser Lys Ile Thr
785 790 795 800

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Gln Ile His Glu Asn Asp Arg Gly Ser Thr His Asp Ser Leu Asn Lys
                805                 810                 815

Lys Leu Cys Gln Lys Val Asn Ile Ser Lys Ile Ile Ser Gln Met Asn
            820                 825                 830

Gln Ile Tyr Glu Thr Ile Asn Glu Asp Gly Asn Gly Phe Lys Ser Ser
        835                 840                 845

Ile Lys Asp Cys Glu Asp Ile Lys Ser Cys Asp Phe Gly Glu Ile Asn
    850                 855                 860

Ser Asn Lys Lys Glu Asn Tyr Asp Pro Ile Gln Asp Pro Cys Thr Leu
865                 870                 875                 880

Val Lys Lys Thr Lys Arg Lys Gly Ser Cys Lys Ala Gly Ser Ser Leu
                885                 890                 895

Ala Gly Ala Lys Asn Arg Cys Gly Leu Gln Leu Thr Asp Ser Ser Gln
            900                 905                 910

Val Gln Ser Val Pro Leu Asp Ser Gly Leu Arg His His Pro Asn Glu
        915                 920                 925

Ala Asp Ser Gly Pro Gly Glu Gln Thr Asn Leu Pro Lys Met Gln Lys
    930                 935                 940

Gln Ser Ala Gly Arg Ser Leu Gly Asp Ala Phe Ser Val Ser Leu Gly
945                 950                 955                 960

Lys Glu Gly Ser Arg Pro Ala Lys Ala Val Ser Lys Met Thr Pro Lys
                965                 970                 975

Ser Lys Lys Arg Lys Leu Pro Leu Gly Cys Ser Pro Glu Thr His Gly
            980                 985                 990

Thr Val Glu Ile Thr Pro Asn Thr  Asp Leu Ala Lys Ala  Val Asp Ser
        995                 1000                1005

Gln Gln  Thr Glu Lys Glu Asn  Tyr Leu Glu Lys Glu  Lys Ile Ala
    1010                1015                1020
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Lys Arg  Lys Pro Asp Phe Cys  Thr Lys Val Leu Lys  Pro Leu Ser
    1025                 1030                 1035

Glu Thr  Cys Ser Ser Asn Ile  Lys Asn Ser Ser Leu  Asp Ser Met
    1040                 1045                 1050

Cys Lys  Ser Ser Leu Pro Leu  Ser Ile Ser Ser Arg  Lys Thr Leu
    1055                 1060                 1065

Met Leu  Glu Glu Ser Ser Ser  Leu Glu Ser Thr Cys  Ile Phe Gln
    1070                 1075                 1080

Val Gly  Asp Ala Ala His Glu  Lys Ile Thr Thr Gly  Thr Arg Asn
    1085                 1090                 1095

Pro His  His Arg Thr Gln Lys  Ser Thr Pro Gly Ser  Arg Thr Ser
    1100                 1105                 1110

Leu Val  Leu Val Asp Thr Ser  Ser Val Ser Asp Thr  Asn Pro Ala
    1115                 1120                 1125

Asn Pro  Glu Asn Glu Ser Glu  Gly Gln Ser Ser His  Pro Met Arg
    1130                 1135                 1140

Arg Lys  Arg Gln Cys Val Pro  Leu Asn Leu Thr Glu  Pro Ser Leu
    1145                 1150                 1155

Arg Ser  Lys Met Arg Arg
    1160
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<210> 17
<211> 1525
<212> DNA
<213> Homo sapiens

<400> 17

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agctgcacca tgccaaataa tcaccaacac ttctacactg ctgaaaaatt accaagacaa    120

caacaaaatg ttagttttag ctttggaaaa tgaaaaatcc aaagtgaaag aagcccaaga    180

tatcatccta cagctgagaa aagaatgtta ctatctcaca tgtcagctat atgcattgaa    240

aggaaaactt acatcacaac aaacagtaga acctgctcag aaccaggaaa tatgttcctc    300
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tggaatggac cccaatagtg atgacagctc cagaaattta tttgtgaagg atttaccgca 360

aattcctctt gaagaaactg aacttccagg acaaggagaa tcatttcaaa tagaagatca 420

gatacctact attcctcaag acacactggg agttgatttt gattcaggtg aagctaagtc 480

tactgataat gtcttaccta gaactgtatc tgttcgtagc agtttaaaga aacattgtaa 540

cagtatatgt cagtttgata gcttggatga ttttgaaacc agtcatttgg cagggaagtc 600

ttttgaattc gaaagagttg gatttttaga cccactagta aacatgcaca tacctgaaaa 660

tgtacaacac aatgcttgtc aatggagcaa ggaccaagtt aacttatcac caaagctgat 720

tcagccagga acgtttacta aaacaaaaga agacatttta gaatctaaat ctgaacaaac 780

taaaagtaag caaagagata cacaagaaag aaaaagagaa gagaaaagaa aagctaacag 840

gagaaaatca aaacgtatgt caaaatataa agagaataaa agcgaaaata aaaaaactgt 900

tccccaaaaa aaaatgcaca aatctgtcag ttccaatgat gcttacaatt ttaatttgga 960

agagggtgtt catcttactc ctttccgaca aaaagtgagc aatgactcta atagagaaga 1020

aaacaacgag tctgaagtga gcctctgtga atcaagtggt tcaggagatg attccgatga 1080

cctctatttg cccacttgca agtacattca gaatcccacg agcaattcag atagaccagt 1140

caccaggcct ctagctaaaa gagcactgaa atacacagat gaaaaagaga cggagggttc 1200

taagccaaca aaaactccta ccactacacc acctgaaact cagcagtcac ctcatcttag 1260

cctgaaggat atcaccaatg tctccttgta tcctgttgtg aaaatcagaa gactttctct 1320

ttctccaaaa aagaataaag caagcccagc agtggctctg cctaaacgta ggtgcacagc 1380

cagcgtgaac tataaggagc ccaccctcgc ttcgaaactg agaagagggg acccttttac 1440

agatttgtgt tttttgaatt ctcctatttt caagcagaaa aaggatttga gacgttctaa 1500

aaaaagtatg aaacaaatac aatga 1525

<210> 18
<211> 511
<212> PRT
<213> Homo sapiens

<400> 18

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Ile Gly Lys Arg Arg Ser Phe Ile Ala Ala Pro Cys Gln Ile Ile Thr
20 25 30

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Asn Thr Ser Thr Leu Leu Lys Asn Tyr Gln Asp Asn Asn Lys Met Leu
        35                  40                  45

Val Leu Ala Leu Glu Asn Glu Lys Ser Lys Val Lys Glu Ala Gln Asp
    50                  55                  60

Ile Ile Leu Gln Leu Arg Lys Glu Cys Tyr Tyr Leu Thr Cys Gln Leu
65                  70                  75                  80

Tyr Ala Leu Lys Gly Lys Leu Thr Ser Gln Gln Thr Val Glu Pro Ala
                85                  90                  95

Gln Asn Gln Glu Ile Cys Ser Ser Gly Met Asp Pro Asn Ser Asp Asp
            100                 105                 110

Ser Ser Arg Asn Leu Phe Val Lys Asp Leu Pro Gln Ile Pro Leu Glu
        115                 120                 125

Glu Thr Glu Leu Pro Gly Gln Gly Glu Ser Phe Gln Ile Glu Asp Gln
    130                 135                 140

Ile Pro Thr Ile Pro Gln Asp Thr Leu Gly Val Asp Phe Asp Ser Gly
145                 150                 155                 160

Glu Ala Lys Ser Thr Asp Asn Val Leu Pro Arg Thr Val Ser Val Arg
                165                 170                 175

Ser Ser Leu Lys Lys His Cys Asn Ser Ile Cys Gln Phe Asp Ser Leu
            180                 185                 190

Asp Asp Phe Glu Thr Ser His Leu Ala Gly Lys Ser Phe Glu Phe Glu
        195                 200                 205

Arg Val Gly Phe Leu Asp Pro Leu Val Asn Met His Ile Pro Glu Asn
    210                 215                 220

Val Gln His Asn Ala Cys Gln Trp Ser Lys Asp Gln Val Asn Leu Ser
225                 230                 235                 240

Pro Lys Leu Ile Gln Pro Gly Thr Phe Thr Lys Thr Lys Glu Asp Ile
                245                 250                 255
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Leu Glu Ser Lys Ser Glu Gln Thr Lys Ser Lys Gln Arg Asp Thr Gln
            260                 265                 270

Glu Arg Lys Arg Glu Glu Lys Arg Lys Ala Asn Arg Arg Lys Ser Lys
        275                 280                 285

Arg Met Ser Lys Tyr Lys Glu Asn Lys Ser Glu Asn Lys Lys Thr Val
    290                 295                 300

Pro Gln Lys Lys Met His Lys Ser Val Ser Ser Asn Asp Ala Tyr Asn
305                 310                 315                 320

Phe Asn Leu Glu Glu Gly Val His Leu Thr Pro Phe Arg Gln Lys Val
                325                 330                 335

Ser Asn Asp Ser Asn Arg Glu Glu Asn Asn Glu Ser Glu Val Ser Leu
            340                 345                 350

Cys Glu Ser Ser Gly Ser Gly Asp Asp Ser Asp Asp Leu Tyr Leu Pro
        355                 360                 365

Thr Cys Lys Tyr Ile Gln Asn Pro Thr Ser Asn Ser Asp Arg Pro Val
    370                 375                 380

Thr Arg Pro Leu Ala Lys Arg Ala Leu Lys Tyr Thr Asp Glu Lys Glu
385                 390                 395                 400

Thr Glu Gly Ser Lys Pro Thr Lys Thr Pro Thr Thr Thr Pro Pro Glu
                405                 410                 415

Thr Gln Gln Ser Pro His Leu Ser Leu Lys Asp Ile Thr Asn Val Ser
            420                 425                 430

Leu Tyr Pro Val Val Lys Ile Arg Arg Leu Ser Leu Ser Pro Lys Lys
        435                 440                 445

Asn Lys Ala Ser Pro Ala Val Ala Leu Pro Lys Arg Arg Cys Thr Ala
    450                 455                 460

Ser Val Asn Tyr Lys Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly
465                 470                 475                 480

Asp Pro Phe Thr Asp Leu Cys Phe Leu Asn Ser Pro Ile Phe Lys Gln
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Lys Lys Asp Leu Arg Arg Ser Lys Lys Ser Met Lys Gln Ile Gln
500 505 510

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<211> 3798
<212> DNA
<213> Homo sapiens

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acaaaaatac taaataattc ttctattttc aaaatatctt taaagcacaa caacagggca 180

ttagctcagg ctcttagtag agaaaaagag aattctcgaa gaattacaac tgaaaagatg 240

ctattgcaaa aagaagtaga gaaactgaat tttgagaaca catttcttcg cctaaagcta 300

aataacttga ataagaagct tatagacata gaagctctca tgaacaataa cttgataact 360

gcaactgaaa tgagcagtct ttctgagttc catcagagtt cctttctact gtcagctagc 420

aagaagaaac gagttagtaa acagtgcaag ttgatgcgtc ttccatttgc aagggttcca 480

ttaacttcaa atgatgatga agatgaagat aaagagaaaa tgcagtgtga caacaatatt 540

aaatcaaaga cattacctga tattccctct tcaggatcaa caacacaacc tttatcaact 600

caggataatt cggaagtgtt atttcttaaa gaaaataatc aaaatgtata tggtttagat 660

gattcagaac atatttcttc tatagttgat gtacctccca gagaaagcca ttcccactca 720

gaccaaagtt ctaagacttc tctaatgagt gagatgagaa acgcccagtc tattggccgc 780

agatgggaga aaccatctcc tagtaatgtg actgaaagga agaagcgtgg gtcatcttgg 840

gaatcaaata atctttctgc agacactccc tgtgcaacag ttttagataa acaacacatt 900

tcaagtccag aattaaattg caataatgag ataaatggtc atactaatga aacaaatact 960

gaaatgcaaa gaaataaaca ggatcttcct ggcttatctt ctgagtctgc cagagaacct 1020

aatgcagagt gcatgaatca aattgaggat aatgatgact ttcaattgca gaaaactgtg 1080

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ggcattaaaa agaaaagtaa taaaaaaaca aatgaacatg gaatgaaaac tttcagaaaa 1200

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tcagatgtcg atattgggga aaagattgaa aacaggacag aaagatctga tgtcctggat 1320

ggcaaaaggg gtgcagaaga tcccggtttt attttcaata atgaacagct ggctcagatg 1380

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caaggtgaca gagaaaatgt actgtgtaat aaaaaggaga aaagaataac aaatgagcaa 1500

gaggaaacat actctttatc ccaaagttca ggtaaatttc accaggagag taaatttgat 1560

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aacctagacg tcacaaatga atttcacaca gccaatcttt ccaccaaaga taatggaaat 1740

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ccctcagagc aaaatgaatc aaacattaat aagcttagaa agaaagtaaa ccggaagaca 1860

gaaataattt ctggaatgaa ccacatgtat gaagataatg ataaagatgt ggtgcatggc 1920

ctaaaaaaag gtaatttttt tttcaaaacc caagaggata aagaacctat ctctgaaaac 1980

atagaagttt ccaaagagct tcaaatccca gctctttcta ctagagataa tgaaaatcaa 2040

tgtgactata ggacccagaa tgtgttgggt ttgcaaaagc agatcaccaa tatgtacccc 2100

gttcagcaaa atgaatcaaa agttaataag aagcttaggc agaaagtaaa tcggaagaca 2160

gaaataattt ctgaagtgaa tcatttagat aatgacaaaa gtatagaata cacagttaaa 2220

agtcactcac tctttttaac gcaaaaagat aaggaaataa tccccggaaa cctagaagac 2280

ccaagtgagt ttgaaacacc tgctctttct accaaagata gtggaaacct gtatgattct 2340

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gaaaccaacc aaatatatga gaatgataac aaaggtgtac atgacctaga aaaagataac 2520

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gaatttcaaa cagttgatct tctcatcaaa gataatggaa atttatgtga ttatgacacc 2640

cagaatatat tggagttgaa aaagtatgtt actgatagga aatctgctga gcaaaatgaa 2700

tcaaaaataa ataagctcag gaataaagtg aattggaaga cagaaataat ttctgaaatg 2760

aaccagatat atgaggataa tgataaagat gcacatgtcc aagaaagcta tacaaaagat 2820

cttgatttta aagtaaataa atctaaacaa aaacttgaat gccaagacat tatcaataaa 2880

cactatatgg aagtcaacag taatgaaaag gaaagttgtg atcaaatttt agattcctac 2940

aaagtagtta aaaaacgtaa gaaagaatca tcatgcaagg caaagaacat tttgacaaaa 3000

gctaagaaca aacttgcttc acagttaaca gaatcttcac agacatctat ctccttagaa 3060

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gaaataaaag aaggagagtg tcaggttaaa aaggtaaata aaatgacatc taagtcaaag 3240

aaaaggaaga cctccataga tccttctcca gagagccatg aagtaatgga aagaatactt 3300

gacagcgttc agggaaagtc tactgtatct gaacaagctg ataaggaaaa caatttggag 3360

aatgagaaaa tggtcaaaaa taagccagac ttttacacaa aggcatttag atctttgtct 3420

gagatacatt cacctaacat acaagattct tcctttgaca gtgttcgtga aggtttagta 3480

cctttgagcg tttcttctgg taaaaatgtg ataataaaag aaaattttgc cttggagtgc 3540

tccccagcct ttcaagtaag tgatgatgag catgagaaga tgaacaagat gaaatttaaa 3600

gtcaaccgga gaacccaaaa atcaggaata ggtgatagac cattacagga cttgtcaaat 3660

accagttttg tttcaaataa cactgctgaa tctgaaaata agtcagaaga tctatcttca 3720

gaacggacaa gcagaagaag aaggtgtact cctttctatt ttaaagagcc aagcctcaga 3780

gacaagatga gaagatga 3798

<210> 20
<211> 1265
<212> PRT
<213> Homo sapiens

<400> 20

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Lys Arg His Leu Lys Asp Lys Arg Ile Ser Lys Thr Thr Lys Leu Asn
20 25 30

Val Ser Leu Ala Ser Lys Ile Lys Thr Lys Ile Leu Asn Asn Ser Ser
35 40 45

Ile Phe Lys Ile Ser Leu Lys His Asn Asn Arg Ala Leu Ala Gln Ala
50 55 60

Leu Ser Arg Glu Lys Glu Asn Ser Arg Arg Ile Thr Thr Glu Lys Met
65 70 75 80

Leu Leu Gln Lys Glu Val Glu Lys Leu Asn Phe Glu Asn Thr Phe Leu
85 90 95

Arg Leu Lys Leu Asn Asn Leu Asn Lys Lys Leu Ile Asp Ile Glu Ala
100 105 110

Leu Met Asn Asn Asn Leu Ile Thr Ala Ile Glu Met Ser Ser Leu Ser
115 120 125

Glu Phe His Gln Ser Ser Phe Leu Leu Ser Ala Ser Lys Lys Lys Arg
130 135 140

Ile Ser Lys Gln Cys Lys Leu Met Arg Leu Pro Phe Ala Arg Val Pro
145 150 155 160

Leu Thr Ser Asn Asp Asp Glu Asp Glu Asp Lys Glu Lys Met Gln Cys
165 170 175

Asp Asn Asn Ile Lys Ser Lys Thr Leu Pro Asp Ile Pro Ser Ser Gly
180 185 190

Arg Thr Thr Gln Pro Leu Ser Thr Gln Asp Asn Ser Gly Val Leu Phe
195 200 205

Leu Lys Glu Asn Asn Gln His Val Tyr Gly Leu Asp Asp Ser Glu His
210 215 220

Ile Ser Ser Ile Val Asp Val Pro Pro Arg Glu Ser His Ser His Ser
225 230 235 240

Asp Gln Ser Ser Lys Thr Ser Leu Met Ser Glu Met Arg Asn Ala Gln
245 250 255

Ser Ile Gly Arg Arg Trp Glu Lys Pro Ser Pro Ser Asn Val Thr Glu
260 265 270

Arg Lys Lys Arg Gly Ser Ser Trp Glu Ser Asn Asn Leu Ser Ala Asp
275 280 285

Thr Pro Cys Ala Thr Val Leu Asp Lys Gln His Ile Ser Ser Pro Glu
290 295 300

Leu Asn Cys Asn Asn Glu Ile Asn Gly His Thr Asn Glu Thr Asn Thr
305 310 315 320

Glu Met Gln Arg Asn Lys Gln Asp Leu Pro Gly Leu Ser Ser Glu Ser
325 330 335

Ala Arg Glu Pro Asn Ala Glu Cys Met Asn Gln Ile Glu Asp Asn Asp
340 345 350

Asp Phe Gln Leu Gln Lys Thr Val Tyr Asp Ala Asp Met Asp Leu Thr
355 360 365

Ala Ser Glu Val Ser Lys Ile Val Thr Val Ser Thr Gly Ile Lys Lys
370 375 380

Lys Ser Asn Lys Lys Thr Asn Glu His Gly Met Lys Thr Phe Arg Lys
385 390 395 400

Val Lys Asp Ser Ser Ser Glu Lys Lys Arg Glu Arg Ser Lys Arg Gln
405 410 415

Phe Lys Asn Ser Ser Asp Val Asp Ile Gly Glu Lys Ile Glu Asn Arg
420 425 430

Thr Glu Arg Ser Asp Val Leu Asp Gly Lys Arg Gly Ala Glu Asp Pro
435 440 445

Gly Leu Phe Phe Asn Asn Glu Gln Leu Ala Gln Met Asn Glu Gln Leu
450 455 460

Ala Gln Val Asn Glu Leu Lys Lys Met Thr Leu Gln Thr Gly Phe Glu
465 470 475 480

Gln Gly Asp Arg Glu Asn Val Leu Cys Asn Lys Lys Glu Lys Arg Val
485 490 495

Thr Asn Glu Gln Glu Glu Thr Tyr Ser Leu Ser Gln Ser Ser Gly Lys
500 505 510

Phe His Gln Glu Ser Lys Phe Asp Lys Gly Gln Asn Ser Leu Thr Cys
515 520 525

Asn Lys Ser Lys Ala Ser Arg Gln Thr Phe Val Ile His Lys Leu Glu
530 535 540

Lys Asp Asn Leu Leu Pro Asn Gln Lys Asp Lys Val Thr Ile Tyr Glu
545 550 555 560

Asn Leu Asp Val Thr Asn Glu Phe His Thr Ala Asn Leu Ser Thr Lys
565 570 575

Asp Asn Gly Asn Leu Cys Asp Tyr Gly Thr His Asn Ile Leu Asp Leu
580 585 590

Lys Lys Tyr Val Thr Asp Ile Gln Pro Ser Glu Gln Asn Glu Ser Asn
595 600 605

Ile Asn Lys Leu Arg Lys Lys Val Asn Arg Lys Thr Glu Ile Ile Ser
610 615 620

Gly Met Asn His Met Tyr Glu Asp Asn Asp Lys Asp Val Val His Gly
625 630 635 640

Leu Lys Lys Gly Asn Phe Phe Phe Lys Thr Gln Glu Asp Lys Glu Pro
645 650 655

Ile Ser Glu Ser Ile Glu Val Ser Lys Glu Leu Gln Ile Pro Ala Leu
660 665 670

Ser Thr Arg Asp Asn Glu Asn Gln Cys Asp Tyr Arg Thr Gln Asn Val
675 680 685

Leu Gly Leu Gln Lys Gln Ile Thr Asn Met Tyr Pro Val Gln Gln Asn
690 695 700

Glu Ser Lys Val Asn Lys Lys Leu Arg Gln Lys Val Asn Arg Lys Thr
705 710 715 720

Glu Ile Ile Ser Glu Val Asn His Leu Asp Asn Asp Lys Ser Ile Glu
725 730 735

Tyr Thr Val Lys Ser His Ser Leu Phe Leu Thr Gln Lys Asp Lys Glu
740 745 750

Ile Ile Pro Gly Asn Leu Glu Asp Pro Ser Glu Phe Glu Thr Pro Ala
755 760 765

Leu Ser Thr Lys Asp Ser Gly Asn Leu Tyr Asp Ser Glu Ile Gln Asn

770 775 780

Val Leu Gly Val Lys His Gly His Asp Met Gln Pro Ala Cys Gln Asn
785 790 795 800

Asp Ser Lys Ile Gly Lys Lys Pro Arg Leu Asn Val Cys Gln Lys Ser
805 810 815

Glu Ile Ile Pro Glu Thr Asn Gln Ile Tyr Glu Asn Asp Asn Lys Gly
820 825 830

Val His Asp Leu Glu Lys Asp Asn Phe Phe Ser Leu Thr Pro Lys Asp
835 840 845

Lys Glu Thr Ile Ser Glu Asn Leu Gln Val Thr Asn Glu Phe Gln Thr
850 855 860

Val Asp Leu Leu Ile Lys Asp Asn Gly Asn Leu Cys Asp Tyr Asp Thr
865 870 875 880

Gln Asn Ile Leu Glu Leu Lys Lys Tyr Val Thr Asp Arg Lys Ser Ala
885 890 895

Glu Gln Asn Glu Ser Lys Ile Asn Lys Leu Arg Asn Lys Val Asn Trp
900 905 910

Lys Thr Glu Ile Ile Ser Glu Met Asn Gln Ile Tyr Glu Asp Asn Asp
915 920 925

Lys Asp Ala His Val Gln Glu Ser Tyr Thr Lys Asp Leu Asp Phe Lys
930 935 940

Val Asn Lys Ser Lys Gln Lys Leu Glu Cys Gln Asp Ile Ile Asn Lys
945 950 955 960

His Tyr Met Glu Val Asn Ser Asn Glu Lys Glu Ser Cys Asp Gln Ile
965 970 975

Leu Asp Ser Tyr Lys Val Val Lys Lys Arg Lys Lys Glu Ser Ser Cys
980 985 990

Lys Ala Lys Asn Ile Leu Thr Lys Ala Lys Asn Lys Leu Ala Ser Gln
995 1000 1005

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Leu Thr  Glu Ser Ser Gln Thr  Ser Ile Ser Leu Glu  Ser Asp Leu
    1010                 1015                 1020

Lys His  Ile Thr Ser Glu Ala  Asp Ser Asp Pro Gly  Asn Pro Val
    1025                 1030                 1035

Glu Leu  Cys Lys Thr Gln Lys  Gln Ser Thr Thr Thr  Leu Asn Lys
    1040                 1045                 1050

Lys Asp  Leu Pro Phe Val Glu  Glu Ile Lys Glu Gly  Glu Cys Gln
    1055                 1060                 1065

Val Lys  Lys Val Asn Lys Met  Thr Ser Lys Ser Lys  Lys Arg Lys
    1070                 1075                 1080

Thr Ser  Ile Asp Pro Ser Pro  Glu Ser His Glu Val  Met Glu Arg
    1085                 1090                 1095

Ile Leu  Asp Ser Val Gln Gly  Lys Ser Thr Val Ser  Glu Gln Ala
    1100                 1105                 1110

Asp Lys  Glu Asn Asn Leu Glu  Asn Glu Lys Met Val  Lys Asn Lys
    1115                 1120                 1125

Pro Asp  Phe Tyr Thr Lys Ala  Phe Arg Ser Leu Ser  Glu Ile His
    1130                 1135                 1140

Ser Pro  Asn Ile Gln Asp Ser  Ser Phe Asp Ser Val  Arg Glu Gly
    1145                 1150                 1155

Leu Val  Pro Leu Ser Val Ser  Ser Gly Lys Asn Val  Ile Ile Lys
    1160                 1165                 1170

Glu Asn  Phe Ala Leu Glu Cys  Ser Pro Ala Phe Gln  Val Ser Asp
    1175                 1180                 1185

Asp Glu  His Glu Lys Met Asn  Lys Met Lys Phe Lys  Val Asn Arg
    1190                 1195                 1200

Arg Thr  Gln Lys Ser Gly Ile  Gly Asp Arg Pro Leu  Gln Asp Leu
    1205                 1210                 1215
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Ser Asn Thr Ser Phe Val Ser Asn Asn Thr Ala Glu Ser Glu Asn
1220 1225 1230

Lys Ser Glu Asp Leu Ser Ser Glu Arg Thr Ser Arg Arg Arg Arg
1235 1240 1245

Cys Thr Pro Phe Tyr Phe Lys Glu Pro Ser Leu Arg Asp Lys Met
1250 1255 1260

Arg Arg
1265

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<400> 21

Met Glu Ser Leu Lys Lys Lys Phe Leu Lys Gln Asn Arg Glu Ile Ile
1 5 10 15

Lys Ile Asn Thr Gln Leu Ser Ile Lys Ile Arg Glu Ser Glu Asn Glu
20 25 30

Ile Gln Asp Leu Ile Gln Glu Asn Phe Thr Leu Lys Ser
35 40 45

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Val Glu Asp Leu Lys Lys Lys Gln Ile Arg Gln Tyr Lys Glu Ile Ile
1 5 10 15

Arg Ile Ser Lys Ala Gln Ser Ile Arg Ile Lys Glu Leu Gln Leu Glu
20 25 30

Asn Glu Arg Leu Leu Ser Glu Asn Ile Asp Leu Arg Thr
35 40 45

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Val Glu Asn Ile Arg Gln Ser Tyr Ser Arg Gln Asn Ser Leu Leu Ala
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Lys Asp Asn Ser Ile Leu Lys Ile Lys Val Asn Ser Leu Glu Lys Lys
20 25 30

Ile Ser Gln Leu Val Gln Glu Asn Val Thr Leu Arg Ser
35 40 45

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<213> Neurospora crassa

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Leu Glu Leu Leu Arg Arg Lys Phe Leu Arg Gln Asn Arg Asp Ile Ala
1 5 10 15

Arg Val Asn Ser Thr Gln Ser Leu Arg Ile Arg Gly Leu Glu Asn Glu
20 25 30

Cys Ala Arg Leu Leu Ser Glu Asn Leu Glu Leu Arg Gly
35 40 45

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Gly Ser Lys Val Glu Gln Gln Tyr Lys Leu Leu Asn Ala Glu Leu Met
1 5 10 15

Asp Gln Val Gln Lys Gln Arg Leu Glu Ile Gly Glu Tyr Arg Lys Arg
20 25 30

Val Ile Ser Leu Glu Arg Glu Ile Met Asp Ile Arg Glu
35 40 45

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Gly Arg Glu Lys Leu Arg Arg Ser Val Lys Val Ile Asn Tyr Ala Ile
1 5 10 15

Pro Ser Leu Arg Thr Lys Leu Arg Arg Asp Phe
20 25

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<400> 27

Pro Asp Gly Arg Ser Arg Arg Glu Arg Lys Lys Val Asn Tyr Ala Leu
1 5 10 15

Pro Gly Leu Arg Thr Lys Leu Arg Arg Asn Phe
20 25

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Ser Phe Thr Arg Thr Arg Arg Thr Arg Gly Lys Ala Val Asp Tyr Thr
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Leu Pro Ser Leu Arg Ala Lys Met Arg Arg Pro Ser
20 25

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Glu Thr Ser Arg Pro Ser Arg Arg Ala Arg Ala Ala Ile Ser Tyr Thr
1 5 10 15

Glu Pro Asn Leu Arg Asp Lys Met Arg Arg Pro Thr
20 25

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Asn Ser Ala Arg Pro Ser Arg Ser Cys Arg Pro Thr Ser Leu Val Glu
1 5 10 15

Pro Ser Leu Lys Asn Lys Leu Arg Asn Gly Ser
20 25

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Thr Val Arg Arg Gln Arg Ser Ala Lys Met Asn Ile Lys Ser Leu Lys
1 5 10 15

Glu Pro Ser Gly Lys Asp Lys Leu Arg Arg Pro Gly
20 25

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Thr Val Gly Arg Pro Ser Arg Gln Ala Ala Glu Lys Ile Lys Ser Tyr
1 5 10 15

Lys Glu Pro Ser Leu Lys Glu Lys Met Arg Gly Gly Phe
20 25

<210> 33
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Ser Val Gly Arg Pro Ser Arg His Ala Ala Glu Lys Val Gln Ser Tyr
1 5 10 15

Arg Glu Val Ser Leu Arg Val Lys Met Arg Arg Lys Cys
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<210> 34
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Ala Val Ala Leu Thr Lys Arg Arg Cys Ser Thr Ile Lys Ser Tyr Lys
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Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly Asp
20 25

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His Pro Met Arg Arg Lys Arg Gln Cys Val Pro Leu Asn Leu Thr Glu
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Pro Ser Leu Arg Ser Lys Met Arg Arg
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<210> 36
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<212> PRT
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Ala Val Ala Leu Pro Lys Arg Arg Cys Thr Ala Ser Val Asn Tyr Lys
1 5 10 15

Glu Pro Thr Leu Ala Ser Lys Leu Arg Arg Gly Asp
20 25

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<400> 37

Ser Glu Arg Thr Ser Arg Arg Arg Arg Cys Thr Pro Phe Tyr Phe Lys
1 5 10 15

Glu Pro Ser Leu Arg Asp Lys Met Arg Arg
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